**Copper ion altered association network among multi-genes and enzyme activity of laccase in *Ganoderma lucidum***

Xincong Kang1,2,3§, Yuewen Chen1,2,3[[1]](#footnote-1)§, Sien Yan2,3, Luman Zeng2,3, Xuehui Liu2,3, Yongquan Hu2,3, Yunlin Wei4, Xiuling Ji4, Dongbo Liu1,2,3,5\*

1 Hunan Provincial Key Laboratory of Crop Germplasm Innovation and Utilization, Hunan Agricultural University, 410128, Changsha, Hunan, P. R. China;

2 State Key Laboratory of Subhealth Intervention Technology, 410128, Changsha, Hunan, P. R. China;

3 Horticulture and Landscape College, Hunan Agricultural University, 410128, Changsha, Hunan, P. R. China;

4 Kunming University of Science and Technology, 650504, Kunming, Yunnan, P.R China;

5 Hunan Co-Innovation Center for Utilization of Botanical Functional Ingredients, 410128, Changsha, Hunan, P. R. China.

\*Address correspondence toDongbo Liu

E-mail: [chinasaga@163.com](mailto:chinasaga@163.com)

Tel/ Fax: 86-731-84635293.

**Table S1 Primer pairs designed for qPCR analysis**

|  |  |  |  |
| --- | --- | --- | --- |
| **Gene** | **Forward** | **Reverse** | **Amplicon length(bp)** |
| *Lacc1* | CCATTCGCTCACCGTCATC | CCTTTGCCTTCGTTGTTGTTC | 165 |
| *Lacc2* | GTTCCTCCACTGCCACATC | CAGAGTTCCTTCCACGAGTC | 117 |
| *Lacc3* | CTTACGGGAAACAAGGGTGAT | TGGAGTGAGGTGGACTTTAGCA | 86 |
| *Lacc4* | TGTGAGCGTTGGCGATGA | CGATGTGGCAATGGAGGAAC | 189 |
| *Lacc5* | ATGCGGTCGTGGTCAATAG | ATGGTGTGGTTCGTCAAGTT | 103 |
| *Lacc6* | CCGCTCATCACAGGGAATAA | CACCGTCCGCCCAGTTC | 136 |
| *Lacc7* | ACGCAAGGCAAACGCTATC | GGCGGTGAGGACAAATGAG | 180 |
| *Lacc8* | TTCACTGGCACGGCTTCT | CGCTGGCAATAGGACACTG | 81 |
| *Lacc9* | AGACGCCCTTCAACATCAAC | GAGACCATACACGCTACCT | 123 |
| *Lacc10* | AGACCGACCTCCATCCTTAC | ATGAAGAAGTCCGTAGTGTTGAAG | 112 |
| *Lacc11* | ATAAGGAGGCGAAGAACACAAC | GGCGACACGGATGAATGAG | 125 |
| *Lacc12* | GCAACGACACTTCATCCAACT | AGGTGACGGAGGAGGTTATG | 105 |
| *Lacc13* | GACAACTTGAGCAATGACACCAT | TGACCATAGCAGGACCATCG | 100 |
| *Lacc14* | TCTGCCTGGTCCGCTTAT | CATCGTGTGGTTCGTGAGTT | 82 |
| *Lacc15* | CAAGCGGTGGACAACTACTG | GTAACGCAGAATCGCAGAGT | 99 |
| *Lacc16* | GCGTGATGTCGTGAACCTT | GATGAGGCAGTGGAGGAAC | 94 |
| *GAPDH* | CGCTCAACAAGAACTTCGTCAA | CGTAGACAAGGAGGTCACAGA | 87 |

**Fig. S1** Time course transcriptional profiles of putative laccase genes in *G. lucidum*. **A)** Transcriptional level of laccase genes at developmental time points under the control condition. **B)** Transcriptional level of laccase genes at developmental time points under Cu2+ stress. Transcript amounts were normalized with the endogenous reference gene *GAPDH* and calculated by 2-△CT, △CT was calculated as (CT target -CT *GAPDH*). The laccase mRNA transcript levels on the 2nd day were absent for the two groups due to insufficient amount of RNA in any type of fungal cultures.

**Fig. S2** Distribution of putative *cis*-acting elements in the promoter region of gene *Lacc1*-*Lacc16* upstream 2000 bp of the start codon. CAAT box（ ）; MRE （ ）; STRE （ ）; CRE（ ）; NIT（ ）; TATA box（ ）; XRE（ ）; ARE（ ）. MRE: Metal responsive element; STRE: stress response element; CRE: cyclic AMP-responsive element; NIT: Nitrogen repression response element; XRE: Xenobiotic response element; ARE: antioxidant responsive element.

1. § Equal contributors [↑](#footnote-ref-1)